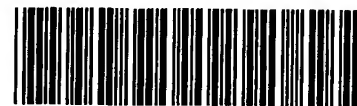


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The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/729,830
Source: JEWO
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PATENT APPLICATION: US/10/729,830

DATE: 10/22/2004

TIME: 14:41:13

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10222004\J729830.raw

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3 <110> APPLICANT: Von der Muelbe, Florian
4      Hoerr, Ingmar
5      Pascolo, Steve
7 <120> TITLE OF INVENTION: Pharmaceutical composition containing a stabilised mRNA
8      optimised for translation in its coding regions
10 <130> FILE REFERENCE: 2793-1-001PCT/CIP
12 <140> CURRENT APPLICATION NUMBER: 10/729,830
13 <141> CURRENT FILING DATE: 2003-12-05
15 <150> PRIOR APPLICATION NUMBER: PCT/EP02/06180
16 <151> PRIOR FILING DATE: 2002-06-05
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 774
24 <212> TYPE: DNA
25 <213> ORGANISM: Influenza virus
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Influenza matrix: wildtype gene (for comparison)
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
32      codon: tga (nucleotides 767 to 769 )
34 <400> SEQUENCE: 1
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36 aggccccctc aaagccgaga tcgcacagag acttgaagat gtctttgcag ggaagaacac 120
37 cgatcttgag gttctcatgg aatggctaaa gacaagacca atcctgtcac ctctgactaa 180
38 ggggatttta ggatttgtgt tcacgctcac cgtgccaggt gagcaggagac tgcagcgtag 240
39 acgctttgtc caaaatgccc ttaatgggaa cgggggatcca aataacatgg acaaagcagt 300
40 taaactgtat aggaagctca agagggagat aacattccat gggggccaaag aaatctcact 360
41 cagttattct gctgggtgcac ttgccagttg tatgggcctc atatacaaca ggatgggggc 420
42 tgtgaccact gaagtggcat ttggcctggt atgtgcaacc tgtgaacaga ttgctgactc 480
43 ccagcatcgg tctcataggc aaatggtgac aacaaccaac ccactaatca gacatgagaa 540
44 cagaatgggt ttagccagca ctacagctaa ggctatggag caaatggctg gatcgagtga 600
45 gcaagcagca gaggccatgg aggttgctag tcaggctagg caaatggtgc aagcgatgag 660
46 aaccattggg actcatccta gctccagtgc tggcttgaaa aatgatcttc ttgaaaattt 720
47 gcaggcctat cagaaacgaa tgggggtgca gatgcaacgg ttcaagtga ctag 774
50 <210> SEQ ID NO: 2
51 <211> LENGTH: 252
52 <212> TYPE: PRT
53 <213> ORGANISM: Influenza virus
55 <400> SEQUENCE: 2
56 Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
57 1          5          10          15
59 Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe

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PATENT APPLICATION: US/10/729,830

DATE: 10/22/2004

TIME: 14:41:13

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60          20          25          30
62 Ala Gly Lys Asn Thr Asp Leu Glu Val Leu Met Glu Trp Leu Lys Thr
63          35          40          45
65 Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
66          50          55          60
68 Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
69 65          70          75          80
71 Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Lys Ala
72          85          90          95
74 Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
75          100          105          110
77 Lys Glu Ile Ser Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
78          115          120          125
80 Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Ala Phe
81          130          135          140
83 Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
84 145          150          155          160
86 Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
87          165          170          175
89 Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
90          180          185          190
92 Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
93          195          200          205
95 Ala Arg Gln Met Val Gln Ala Met Arg Thr Ile Gly Thr His Pro Ser
96          210          215          220
98 Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
99 225          230          235          240
101 Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
102          245          250
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 775
107 <212> TYPE: DNA
108 <213> ORGANISM: Artificial Sequence
110 <220> FEATURE:
111 <223> OTHER INFORMATION: Description of Artificial Sequence: Influenza
112 matrix: gene with increased G/C-content
114 <220> FEATURE:
115 <223> OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
116 codon: tga (nucleotides 767 to 769)
118 <400> SEQUENCE: 3
119 agatctaaag atgagcctgc tgaccgaggt ggagacctac gtgctgagca tcatccccag 60
120 cgccccctcg aaggccgaga tcgccagag gctggaggac gtgttcgccc gcaagaacac 120
121 cgacctggag gtgctgatgg agtggtgaa gaccaggccc atcctgagcc ccctgaccaa 180
122 gggcatcctg ggcttcgtgt tcacctgac cgtgcccgag gagcgcgccc tgcagcgccc 240
123 ccgcttcgtg cagaacgccc tgaacggcaa cggcgacccc aacaacatgg acaaggccgt 300
124 gaagctgtac aggaagctga agagggagat caccttccac ggcgccaagg agatcagcct 360
125 gagctacagc gccggcgccc tggccagctg catgggcctg atctacaaca ggatgggcgc 420
126 cgtgaccacc gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag 480
127 ccagcacccg agccacaggg agatggtgac caccaccaac ccctgatca ggcacgagaa 540

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PATENT APPLICATION: US/10/729,830

DATE: 10/22/2004

TIME: 14:41:13

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128 caggatggtg ctggccagca ccaccgcca ggccatggag cagatggccg gcagcagcga 600
129 gcaggccgcc gaggccatgg aggtggccag ccaggccagg cagatggtgc aggccatgag 660
130 gaccatcggc acccacccca gcagcagcgc cggcctgaag aacgacctgc tggagaacct 720
131 gcaggcctac cagaagcgca tgggcgtgca gatgcagcgc ttcaagtga ctagt 775
134 <210> SEQ ID NO: 4
135 <211> LENGTH: 844
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence
139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence: Influenza
141 matrix: gene for secreted form (with N-terminal
142 signal sequence) with increased G/C-content
144 <220> FEATURE:
145 <223> OTHER INFORMATION: Start codon: atg (nucleotides 11 to 13), stop
146 codon: tga (nucleotides 836 to 838)
148 <400> SEQUENCE: 4
149 agatctaaag atggcgtca tggcccccg caccctggtg ctgctgctga gcggcgccct 60
150 ggccctgacc cagacctggg ctagcctgct gaccgaggtg gagacctacg tgctgagcat 120
151 catccccagc ggccccctga aggccagat cgcccagagg ctggaggacg tgctcgcccg 180
152 caagaacacc gacctggagg tgctgatgga gtggctgaag accaggccca tcctgagccc 240
153 cctgaccaag ggcacctgg gcttcgtgt caccctgacc gtgcccagcg agcgcgccct 300
154 gcagcgcccg cgcttcgtgc agaagccct gaacggcaac ggcgaccca acaacatgga 360
155 caaggccgtg aagctgtaca ggaagctgaa gagggagatc accttcacg gcgccaagga 420
156 gatcagcctg agctacagcg ccggcgccct ggccagctgc atgggcctga tctacaacag 480
157 gatgggccc gtgaccaccg aggtggcctt cggcctggtg tgcgccacct gcgagcagat 540
158 cgccgacagc cagcaccgca gccacaggca gatggtgacc accaccaacc ccctgatcag 600
159 gcacgagaac aggatggtgc tggccagcac caccgccaag gccatggagc agatggcccg 660
160 cagcagcgag caggccgccc aggccatgga ggtggccagc caggccaggc agatggtgca 720
161 ggccatgagg accatcggca cccaccccag cagcagcgcc ggctgaaga acgacctgct 780
162 ggagaacctg caggcctacc agaagcgcat gggcgtgcag atgcagcgct tcaagtgaac 840
163 tagt 844
166 <210> SEQ ID NO: 5
167 <211> LENGTH: 942
168 <212> TYPE: RNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Description of Artificial Sequence: Influenza
173 matrix: mRNA with stabilisation sequences
175 <220> FEATURE:
176 <223> OTHER INFORMATION: The stabilisation sequences are derived from 5'-
177 and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
178 respectively.
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
182 codon: uga (nucleotides 812 to 814)
184 <400> SEQUENCE: 5
185 gcuuguucuu uuugcagaag cucagaauaa acgcucaacu uuggcagauc uaaagaugag 60
186 ucuucuaacc gagguagaaa cguacguucu cucuaucac cgcucaggcc ccucaaagc 120
187 cgagaucgca cagagacuug aagaugucuu ugcagggaag aacaccgauc uagagguicu 180

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RAW SEQUENCE LISTING

DATE: 10/22/2004

PATENT APPLICATION: US/10/729,830

TIME: 14:41:13

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188 cauggaaugg cuaaagacaa gaccaauccu gucaccucug acuaagggga uuuuaggauu 240
189 uguguucacg cucaccgugc ccagugagcg aggacugcag cguagacgcu uuguccaaaa 300
190 ugcccuuaau gggaacgggg auccaaauaa cauggacaaa gcaguuaaac uguauaggaa 360
191 gcucaagagg gagauaacau uccauggggc caaagaaauc ucacucaguu auucugcugg 420
192 ugcacuugcc aguuguaugg gccucauaa caacaggau ggggcuguga ccacugaagu 480
193 ggcauuuggc cugguaugug caaccuguga acagaugcu gacucccagc aucggucuca 540
194 uaggcaaaug gugacaacaa ccaaccacac auacagacau gagaacagaa ugguuuagc 600
195 cagcacuaca gcuaaggcua uggagcaaa ggcuggaucg agugagcaag cagcagaggc 660
196 cauggagguu gcuagucagg cuaggcaaa ggugcaagcg augagaacca uugggacuca 720
197 uccuagcucc agugcugguc ugaaaaauga ucuucuugaa aaauugcagg ccuacagaa 780
198 acgaaugggg gugcagaugc aacgguucaa gugaacuagu gacugacuag cccgcugggc 840
199 cucccaacgg gccuccucc ccuccuugca ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
200 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 942
203 <210> SEQ ID NO: 6
204 <211> LENGTH: 942
205 <212> TYPE: RNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Artificial Sequence: Influenza
210 matrix: mRNA with increased G/C-content and
211 stabilisation sequences
213 <220> FEATURE:
214 <223> OTHER INFORMATION: The stabilisation sequences are derived from 5'-
215 and 3'-UTRs of a-globin-mRNA from Xenopus laevis,
216 respectively.
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
220 codon: uga (nucleotides 812 to 814)
222 <400> SEQUENCE: 6
223 gcuuguucuu uuugcagaag cucagaauaa acgcucaacu uuggcagauc uaaagaugag 60
224 ccugcugacc gagguggaga ccuacgugcu gagcaucauc cccagcggcc ccuagaaggc 120
225 cgagaucgcc cagaggcugg aggacguguu cgccggcaag aacaccgacc uggaggugcu 180
226 gauggagugg cugaagacca ggcccauccu gagccccug accaagggca uccugggcuu 240
227 cguguucacc cugaccgugc ccagcgagcg cggccugcag cgccgccgcu ucgugcagaa 300
228 cgcccugaac ggcaacggcg accccaacaa cauggacaa gcccugaagc uguacaggaa 360
229 gcugaagagg gagaucaccu uccacggcgc caaggagau agccugagcu acagcgccgg 420
230 cgcccuggcc agcugcaugg gccugaucua caacaggau ggcgccguga ccaccgaggu 480
231 ggccuucggc cuggugugcg ccaccugcga gcagaucgcc gacagccagc accgcagcca 540
232 caggcagaug gugaccacca ccaacccccc gaucaggcac gagaacagga uggugcuggc 600
233 cagcaccacc gccaaaggcca uggagcagau ggccggcagc agcgagcagg ccgccgaggc 660
234 cauggaggug gccagccagg ccaggcagau ggugcaggcc augaggacca ucggcaccca 720
235 ccccgagcag agcgccggcc ugaagaacga ccugcuggag aaccugcagg ccuaccagaa 780
236 gcgcaugggc gugcagaugc agcgcuucaa gugaacuagu gacugacuag cccgcugggc 840
237 cucccaacgg gccuccucc ccuccuugca ccaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
238 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 942
241 <210> SEQ ID NO: 7
242 <211> LENGTH: 1011
243 <212> TYPE: RNA
244 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING

DATE: 10/22/2004

PATENT APPLICATION: US/10/729,830

TIME: 14:41:13

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\10222004\J729830.raw

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246 <220> FEATURE:
247 <223> OTHER INFORMATION: Description of Artificial Sequence: Influenza
248     matrix: mRNA coding for secreted form with
249     increased G/C-content and stabilisation sequences
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Start codon: aug (nucleotides 56 to 58), stop
253     codon: uga (nucleotides 881 to 883)
255 <400> SEQUENCE: 7
256 gcuuguucuu uuugcagaag cucagaauaa acgcucaacu uuggcagauc uaaagauggc 60
257 cgucauggcc ccccgacccc uggugcugcu gcugagcggc gcccuggccc ugacccagac 120
258 cugggccagc cugcugaccg agguggagac cuacgugcug agcaucaucc ccagcggccc 180
259 ccugaaggcc gagaucgccc agaggcugga ggacguguuc gccggcaaga acaccgaccu 240
260 ggaggugcug auggaguggc ugaagaccag gcccauccug agccccuga ccaagggcau 300
261 ccugggcuuu guguucaccc ugaccgugcc cagcgagcgc ggccugcagc gccgccguu 360
262 cgugcagaac gcccugaacg gcaacggcga cccaacaac auggacaagg ccgugaagcu 420
263 guacaggaag cugaagaggg agaucacuu ccacggcgcc aaggagauca gccugagcua 480
264 cagcgccggc gcccuggcca gcugcauggg ccugaucuaa aacaggauug gcgccgugac 540
265 caccgaggug gccuucggcc uggugugcgc caccugcgag cagaucgccg acagccagca 600
266 ccgcagccac aggcagaugg ugaccaccac caacccccug aucaggcacg agaacaggau 660
267 ggugcuggcc agcaccaccg ccaaggccau ggagcagaug gccggcagca gcgagcaggc 720
268 cgccgaggcc auggaggugg ccagccaggc caggcagaug gugcaggcca ugaggaccu 780
269 cggcaccac cccagcagca gcgcccggcu gaagaacgac cugcuggaga accugcaggc 840
270 cuaccagaag cgcauggggc ugcagaugca gcgcuucaag ugaacuagug acugacuagc 900
271 ccgcugggcc uccaacggg ccuccuccc cuccuugcac caaaaaaaaa aaaaaaaaaa 960
272 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a          1011
275 <210> SEQ ID NO: 8
276 <211> LENGTH: 940
277 <212> TYPE: DNA
278 <213> ORGANISM: Homo sapiens
280 <220> FEATURE:
281 <223> OTHER INFORMATION: MAGE1: wildtype-gene (for comparison)
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Start codon: atg (nucleotides 5 to 7), stop codon:
285     tga (nucleotides 932 to 934)
287 <400> SEQUENCE: 8
288 catcatgtct cttgagcaga ggagtctgca ctgcaagcct gaggaagccc ttgaggccca 60
289 acaagaggcc ctgggctggg tgtgtgtgca ggctgccacc tcctcctcct ctctctgtgt 120
290 cctgggcacc ctggaggagg tgcccactgc tgggtcaaca gatcctcccc agagtcctca 180
291 gggagcctcc gcctttccca ctaccatcaa cttcactcga cagaggcaac ccagtgaggg 240
292 ttccagcagc cgtgaagagg aggggccaag cacctcttgt atcctggagt ccttgttccg 300
293 agcagtaatc actaagaagg tggctgattt ggttggtttt ctgctcctca aatatcgagc 360
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VERIFICATION SUMMARY

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TIME: 14:41:14

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